



<110> SAITO, Shuji
TSUZAKI, Yoshinari
YANAGIDA, Noboru

<120> NOVEL FUSED PROTEIN, GENE THEREFOR, RECOMBINANT VECTOR,
RECOMBINANT VIRUS, AND ITS USE

<130> 981167

<140> 09/147,052
<141> 1999-04-05

<150> JP 08-103548
<151> 1996-03-29

<150> PCT/JP97/01084
<151> 1997-03-28

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<170> PatentIn Ver. 2.1

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Val Val Ser Ser Val Gln Leu Ser Glu Glu Glu Ser Thr Phe Tyr Leu
35 40 45

Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Phe Gly Cys
50 55 60

Met Ser Ile Thr Lys Lys Asp Ala Asn Pro Asn Asn Gly Gln Thr Gln
65 70 75 80

Leu Glu Ala Ala Arg Met Glu Leu Thr Asp Leu Ile Asn Ala Lys Ala
85 90 95

Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala Lys Ile Glu Ala Ser Leu
100 105 110

Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val Asn Asn Asn Leu Asn Ala
115 120 125

Thr Leu Glu Gln Leu Lys Met Ala Lys Thr Asn Leu Glu Ser Ala Ile
130 135 140

Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe Asp Asn Glu His Pro Asn
145 150 155 160

Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr Thr Leu Glu Gln Arg Ala
165 170 175

Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala Tyr Asn Gln Ile Arg Asn
180 185 190

Asn Leu Val Asp Leu Tyr Asn Lys Ala Ser Ser Leu Ile Thr Lys Thr
195 200 205

Leu Asp Pro Leu Asn Gly Gly Thr Leu Leu Asp Ser Asn Glu Ile Thr
210 215 220

Thr Ala Asn Lys Asn Ile Asn Asn Thr Leu Ser Thr Ile Asn Glu Gln
225 230 235 240

Lys Thr Asn Ala Asp Ala Leu Ser Asn Ser Phe Ile Lys Lys Val Ile
245 250 255

Gln Asn Asn Glu Gln Ser Phe Val Gly Thr Phe Thr Asn Ala Asn Val
260 265 270

Gln Pro Ser Asn Tyr Ser Phe Val Ala Phe Ser Ala Asp Val Thr Pro
275 280 285

Val Asn Tyr Lys Tyr Ala Arg Arg Thr Val Trp Asn Gly Asp Glu Pro
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Ser Ser Arg Ile Leu Ala Asn Thr Asn Ser Ile Thr Asp Val Ser Trp
305 310 315 320

Ile Tyr Ser Leu Ala Gly Thr Asn Thr Lys Tyr Gln Phe Ser Phe Ser
325 330 335

Asn Tyr Gly Pro Ser Thr Gly Tyr Leu Tyr Phe Pro Tyr Lys Leu Val
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Lys Ala Ala Asp Ala Asn Asn Val Gly Leu Gln Tyr Lys Leu Asn Asn
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Gly Asn Val Gln Gln Val Glu Phe Ala Thr Ser Thr Ser Ala Asn Asn
370 375 380

Thr Thr Ala Asn Pro Thr Pro Ala Val Asp Glu Ile Lys Val Ala Lys
385 390 395 400

Ile Val Leu Ser Gly Leu Arg Phe Gly Gln Asn Thr Ile Glu Leu Ser
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Val Pro Thr Gly Glu Gly Asn Met Asn Lys Val Ala Pro Met Ile Gly
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Val Val Ser Ser Val Gln Leu Ser Glu Glu Ser Thr Phe Tyr Leu
 35 40 45

Cys Pro Pro Pro Val Gly Ser Thr Val Ile Arg Leu Glu Pro Pro Arg
 50 55 60

Lys Cys Pro Glu Pro Arg Lys Ala Thr Glu Trp Gly Glu Gly Ile Ala
 65 70 75 80

Ile Leu Phe Lys Glu Asn Ile Ser Pro Tyr Lys Phe Lys Val Thr Leu
 85 90 95

Tyr Tyr Lys Asn Ile Ile Gln Thr Thr Trp Thr Gly Thr Thr Tyr
 100 105 110

Arg Gln Ile Thr Asn Arg Tyr Thr Asp Arg Thr Pro Val Ser Ile Glu

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Glu Ile Thr Asp Leu Ile Asp Gly Lys Gly Arg Cys Ser Ser Lys Ala		
130	135	140
Arg Tyr Leu Arg Asn Asn Val Tyr Val Glu Ala Phe Asp Arg Asp Ala		
145	150	155
Gly Glu Lys Gln Val Leu Leu Lys Pro Ser Lys Phe Asn Thr Pro Glu		
165	170	175
Ser Arg Ala Trp His Thr Thr Asn Glu Thr Tyr Thr Val Trp Gly Ser		
180	185	190
Pro Trp Ile Tyr Arg Thr Gly Thr Ser Val Asn Cys Ile Val Glu Glu		
195	200	205
Met Asp Ala Arg Ser Val Phe Pro Tyr Ser Tyr Phe Ala Met Ala Asn		
210	215	220
Gly Asp Ile Ala Asn Ile Ser Pro Phe Tyr Gly Leu Ser Pro Pro Glu		
225	230	235
Ala Ala Ala Glu Pro Met Gly Tyr Pro Gln Asp Asn Phe Lys Gln Leu		
245	250	255
Asp Ser Tyr Phe Ser Met Asp Leu Asp Lys Arg Arg Lys Ala Ser Leu		
260	265	270
Pro Val Lys Arg Asn Phe Leu Ile Thr Ser His Phe Thr Val Gly Trp		
275	280	285
Asp Trp Ala Pro Lys Thr Thr Arg Val Cys Ser Met Thr Lys Trp Lys		
290	295	300
Glu Val Thr Glu Met Leu Arg Ala Thr Val Asn Gly Arg Tyr Arg Phe		
305	310	315
Met Ala Arg Glu Leu Ser Ala Thr Phe Ile Ser Asn Thr Thr Glu Phe		
325	330	335
Asp Pro Asn Arg Ile Ile Leu Gly Gln Cys Ile Lys Arg Glu Ala Glu		
340	345	350
Ala Ala Ile Glu Gln Ile Phe Arg Thr Lys Tyr Asn Asp Ser His Val		
355	360	365
Lys Val Gly His Val Gln Tyr Phe Leu Ala Leu Gly Gly Phe Ile Val		

370	375	380
Ala Tyr Gln Pro Val Leu Ser Lys Ser Leu Ala His Met Tyr Leu Arg		
385	390	395
Glu Leu Met Arg Asp Asn Arg Thr Asp Glu Met Leu Asp Leu Val Asn		
405	410	415
Asn Lys His Ala Ile Tyr Lys Lys Asn Ala Thr Ser Leu Ser Arg Leu		
420	425	430
Arg Arg Asp Ile Arg Asn Ala Pro Asn Arg Lys Ile Thr Leu Asp Asp		
435	440	445
Thr Thr Ala Ile Lys Ser Thr Ser Ser Val Gln Phe Ala Met Leu Gln		
450	455	460
Phe Leu Tyr Asp His Ile Gln Thr His Ile Asn Asp Met Phe Ser Arg		
465	470	475
Ile Ala Thr Ala Trp Cys Glu Leu Gln Asn Arg Glu Leu Val Leu Trp		
485	490	495
His Glu Gly Ile Lys Ile Asn Pro Ser Ala Thr Ala Ser Ala Thr Leu		
500	505	510
Gly Arg Arg Val Ala Ala Lys Met Leu Gly Asp Val Ala Ala Val Ser		
515	520	525
Ser Cys Thr Ala Ile Asp Ala Glu Ser Val Thr Leu Gln Asn Ser Met		
530	535	540
Arg Val Ile Thr Ser Thr Asn Thr Cys Tyr Ser Arg Pro Leu Val Leu		
545	550	555
Phe Ser Tyr Gly Glu Asn Gln Gly Asn Ile Gln Gly Gln Leu Gly Glu		
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Asn Asn Glu Leu Leu Pro Thr Leu Glu Ala Val Glu Pro Cys Ser Ala		
580	585	590
Asn His Arg Arg Tyr Phe Leu Phe Gly Ser Gly Tyr Ala Leu Phe Glu		
595	600	605
Asn Tyr Asn Phe Val Lys Met Val Asp Ala Ala Asp Ile Gln Ile Ala		
610	615	620
Ser Thr Phe Val Glu Leu Asn Leu Thr Leu Leu Glu Asp Arg Glu Ile		

625	630	635	640
Leu Pro Leu Ser Val Tyr Thr Lys Glu Glu Leu Arg Asp Val Gly Val			
645	650	655	
Leu Asp Tyr Ala Glu Val Ala Arg Arg Asn Gln Leu His Glu Leu Lys			
660	665	670	
Phe Tyr Asp Ile Asn Lys Val Ile Glu Val Asp Thr Asn Tyr Ala Gly			
675	680	685	
Leu Gln Glu Phe Gly Cys Met Ser Ile Thr Lys Lys Asp Ala Asn Pro			
690	695	700	
Asn Asn Gly Gln Thr Gln Leu Glu Ala Ala Arg Met Glu Leu Thr Asp			
705	710	715	720
Leu Ile Asn Ala Lys Ala Met Thr Leu Ala Ser Leu Gln Asp Tyr Ala			
725	730	735	
Lys Ile Glu Ala Ser Leu Ser Ser Ala Tyr Ser Glu Ala Glu Thr Val			
740	745	750	
Asn Asn Asn Leu Asn Ala Thr Leu Glu Gln Leu Lys Met Ala Lys Thr			
755	760	765	
Asn Leu Glu Ser Ala Ile Asn Gln Ala Asn Thr Asp Lys Thr Thr Phe			
770	775	780	
Asp Asn Glu His Pro Asn Leu Val Glu Ala Tyr Lys Ala Leu Lys Thr			
785	790	795	800
Thr Leu Glu Gln Arg Ala Thr Asn Leu Glu Gly Leu Ser Ser Thr Ala			
805	810	815	
Tyr Asn Gln Ile Arg Asn Asn Leu Val Asp Leu Tyr Asn Lys Ala Ser			
820	825	830	
Ser Leu Ile Thr Lys Thr Leu Asp Pro Leu Asn Gly Gly Thr Leu Leu			
835	840	845	
Asp Ser Asn Glu Ile Thr Thr Ala Asn Lys Asn Ile Asn Asn Thr Leu			
850	855	860	
Ser Thr Ile Asn Glu Gln Lys Thr Asn Ala Asp Ala Leu Ser Asn Ser			
865	870	875	880
Phe Ile Lys Lys Val Ile Gln Asn Asn Glu Gln Ser Phe Val Gly Thr			

885

890

895

Phe Thr Asn Ala Asn Val Gln Pro Ser Asn Tyr Ser Phe Val Ala Phe
900 905 910

Ser Ala Asp Val Thr Pro Val Asn Tyr Lys Tyr Ala Arg Arg Thr Val
915 920 925

Trp Asn Gly Asp Glu Pro Ser Ser Arg Ile Leu Ala Asn Thr Asn Ser
930 935 940

Ile Thr Asp Val Ser Trp Ile Tyr Ser Leu Ala Gly Thr Asn Thr Lys
945 950 955 960

Tyr Gln Phe Ser Phe Ser Asn Tyr Gly Pro Ser Thr Gly Tyr Leu Tyr
965 970 975

Phe Pro Tyr Lys Leu Val Lys Ala Ala Asp Ala Asn Asn Val Gly Leu
980 985 990

Gln Tyr Lys Leu Asn Asn Gly Asn Val Gln Gln Val Glu Phe Ala Thr
995 1000 1005

Ser Thr Ser Ala Asn Asn Thr Thr Ala Asn Pro Thr Pro Ala Val Asp
1010 1015 1020

Glu Ile Lys Val Ala Lys Ile Val Leu Ser Gly Leu Arg Phe Gly Gln
1025 1030 1035 1040

Asn Thr Ile Glu Leu Ser Val Pro Thr Gly Glu Gly Asn Met Asn Lys
1045 1050 1055

Val Ala Pro Met Ile Gly Asn Ile Tyr Leu Ser Ser Asn Glu Asn Asn
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Ala Asp Lys Ile Pro Gly Tyr Arg Arg Pro Gly Thr Phe Leu
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: modification
of Davidson's promoter

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aaaaactatt ctaatttatt gcactc 86

<210> 6
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<223> Description of Artificial Sequence: modification
of Davidson's promoter

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<210> 7
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HindIII-PstI site of modified pUC18

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<210> 8
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<212> DNA
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